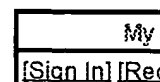
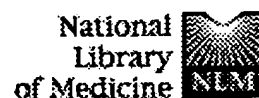


	Type	L #	Hits	Search Text
1	BRS	L1	6405	pyrococcus horikoshi
2	BRS	L2	73472	pyrococcus (ln) horikoshi
3	BRS	L3	17	pyrococcus near1 horikoshi
4	BRS	L4	198	pyrococcus near1 horikoshii
5	BRS	L5	168	"15" and aminotransferase
6	BRS	L6	0	"15" near10 aminotransferase
7	BRS	L7	0	14 near10 aminotransferase
8	BRS	L8	1	14 near20 aminotransferase

(FILE 'HOME' ENTERED AT 17:55:22 ON 10 AUG 2005)

FILE 'AGRICOLA, MEDLINE, CAPLUS, BIOSIS' ENTERED AT 17:55:25 ON 10 AUG
2005

L1	663 S PYROCOCBUS (2N) HORIKOSHII
L2	15 S L1 AND AMINOTRANSFERASE
L3	9 DUP REM L2 (6 DUPLICATES REMOVED)
L4	0 S L3 AND PY<1999



All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Etc

Search PubMed for 2.6.1.57[EC/RN Number] Preview Go C

☒ Limits Preview/Index History Clipboard Details

Limits: Publication Date to 1998

- Search History will be lost after eight hours of inactivity.
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- Search numbers may not be continuous; all searches are represented.
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#26	Search 2.6.1.57[EC/RN Number] Field: All Fields, Limits: Publication Date to 1998	17:54:16	29
#25	Search 2.6.1.57[EC/RN Number] Limits: ignored	17:54:09	37
#23	Search Pyrococcus horikoshii Limits: Publication Date to 1998	17:52:49	7
#21	Search kawarabayasi pyrococcus Field: All Fields, Limits: Publication Date to 1998	17:52:18	3
#20	Search kawarabayasi pyrococcus	17:52:10	20
#19	Search kawarabayasi	17:52:03	69
#13	Search pyrococcus horikoshii aminotransferase	17:51:32	3
#18	Related Articles for PubMed (Select 10671523)	17:50:42	191
#17	Search pyrococcus horikoshii aminotransferase kawarabayasi	17:50:33	1
#12	Search pyrococcus horikoshii	17:48:27	161
#11	Search pyrococcus horikoshi	17:48:21	2
#10	Search kurabayashi tanaka mercury	16:14:08	1
#9	Search kurabayashi tanaka	16:14:01	88
#8	Search carroll minton	16:13:34	3
#6	Search carroll and minton	14:46:37	3
#5	Search (deinococcus [ti] OR radiodurans [ti])	14:23:00	326
#4	Search deinococcus bioremediation	14:21:16	7
#3	Search deinococcus radiodurans bioremediation	14:21:04	7
#1	Search ferreira deinococcus	14:20:31	1

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Jul 26 2005 04:43:15

RESULT 1

```

ID      059096      PRELIMINARY;      PRT;      389 AA.
AC      059096;
DT      01-AUG-1998 (TrEMBLrel. 07, Created)
DT      01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      389aa long hypothetical aspartate aminotransferase.
GN      OrderedLocusNames=PH1371;
OS      Pyrococcus horikoshii.
OC      Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC      Pyrococcus.
OX      NCBI_TaxID=53953;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=OT3;
RX      MEDLINE=98344137; PubMed=9679194;
RA      Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA      Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA      Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA      Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA      Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA      Masuchi Y., Shizuya H., Kikuchi H.;
RT      "Complete sequence and gene organization of the genome of a hyper-
RT      thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL      DNA Res. 5:55-76(1998).
CC      -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC      -!- SIMILARITY: Belongs to the class-I pyridoxal-phosphate-dependent
CC      aminotransferase family.
DR      EMBL; AP000006; BAA30477.1; -.
DR      PIR; E71009; E71009.
DR      PDB; 1DJU; X-ray; A/B=2-389.
DR      PDB; 1GD9; X-ray; A/B=1-389.
DR      PDB; 1GDE; X-ray; A/B=1-389.
DR      GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . . ; IEA.
DR      GO; GO:0008483; F:transaminase activity; IEA.
DR      GO; GO:0009058; P:biosynthesis; IEA.
DR      InterPro; IPR001176; ACC_synthase.
DR      InterPro; IPR004839; Aminotrans_I/II.
DR      InterPro; IPR004838; NHtransf_1_BS.
DR      Pfam; PF00155; Aminotran_1_2; 1.
DR      PRINTS; PR00753; ACCSYNTHASE.
DR      PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW      Aminotransferase; Complete proteome; Hypothetical protein;
KW      Pyridoxal phosphate; Transferase.
SQ      SEQUENCE      389 AA;  43900 MW;  F2A3E919F0C2A7FF CRC64;

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Query Match          100.0%;  Score 1985;  DB 2;  Length 389;
Best Local Similarity 100.0%;  Pred. No. 1e-130;
Matches 389;  Conservative 0;  Mismatches 0;  Indels. 0;  Gaps 0;
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Qy      1  MALSDRLELVSASEIRKLFIDIAAGMKDVISLGIGEPDFDTPQHKEYAKEALDKGLTHYG  60
      |||
Db      1  MALSDRLELVSASEIRKLFIDIAAGMKDVISLGIGEPDFDTPQHKEYAKEALDKGLTHYG  60
      |||
Qy     61  PNIGLLELREAIAEKLKKQNGIEADPKTEIMVLLGANQAFMLGLSAFLKDGEEVLIPTPA 120
      |||

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Db 61 PNIGLLELREAIAEKLKKQNGIEADPKTEIMVLLGANQAFMLGLSAFLKDGEEVLIPTPA 120
 Qy 121 FVSYPAPAVILAGGKPEVPTYEEDFRLNVDELKKYVTDKTRALIINSPCNPTGAVLTKK 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 FVSYPAPAVILAGGKPEVPTYEEDFRLNVDELKKYVTDKTRALIINSPCNPTGAVLTKK 180
 Qy 181 DLEEIADFVVEHDLIVISDEVYEHFIYDDARHYSIASLDGMFERTITVNGFSKTFAMTGW 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 DLEEIADFVVEHDLIVISDEVYEHFIYDDARHYSIASLDGMFERTITVNGFSKTFAMTGW 240
 Qy 241 RLGfVAAPSWIIERMVKFQMYNATCPVTFIQYAAAKALKDERSWKAVEEMRKEYDRRRKL 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 RLGfVAAPSWIIERMVKFQMYNATCPVTFIQYAAAKALKDERSWKAVEEMRKEYDRRRKL 300
 Qy 301 VWKRLNEMGLPTVKPKGAFYIFPRIRDTGLTSKKFSELMLKEARVAVVPGSAFGKAGEGY 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 VWKRLNEMGLPTVKPKGAFYIFPRIRDTGLTSKKFSELMLKEARVAVVPGSAFGKAGEGY 360
 Qy 361 VRISYATAYEKL EAMDRMervLKERKLV 389
 ||||||||||||||||||||
 Db 361 VRISYATAYEKL EAMDRMervLKERKLV 389

RESULT 1

E71009

probable aromatic-amino-acid transaminase (EC 2.6.1.57) PH1371 [similarity] -
Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004

C;Accession: E71009

R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.; Hosoyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.; Nakazawa, H.; Takamiya, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.; Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H. DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3.

A;Reference number: A71000; MUID:98344137; PMID:9679194

A;Accession: E71009

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-389 <KAW>

A;Cross-references: UNIPROT:O59096; GB:AP000006; NID:g3236133; PIDN:BAA30477.1; PID:g3257794

A;Experimental source: strain OT3

A;Note: this accession replaces an interim accession for a sequence replaced by GenBank

C;Genetics:

A;Gene: PH1371

C;Keywords: aminotransferase; phosphoprotein; pyridoxal phosphate

F;233/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 100.0%; Score 1985; DB 2; Length 389;
Best Local Similarity 100.0%; Pred. No. 4.4e-135;
Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MALSDRLELVSASEIRKLF	DIAAGMKDVISLGIGEPD	FDTPQHIKEYAKEALDKGL	THYG	60
Db	1	MALSDRLELVSASEIRKLF	DIAAGMKDVISLGIGEPD	FDTPQHIKEYAKEALDKGL	THYG	60
Qy	61	PNIGLLELREAIAEKLKKQ	NGIEADPKTEIMVLLGANQ	AFMLGLSAFLKDGEEVL	IPTPA	120
Db	61	PNIGLLELREAIAEKLKKQ	NGIEADPKTEIMVLLGANQ	AFMLGLSAFLKDGEEVL	IPTPA	120
Qy	121	FVSYAPAVILAGGKPVEV	PPTYEEDEFRLNVDELKKY	VTDKTRALIINSPCNPTG	AVLTKK	180
Db	121	FVSYAPAVILAGGKPVEV	PPTYEEDEFRLNVDELKKY	VTDKTRALIINSPCNPTG	AVLTKK	180
Qy	181	DLEEIADFVVEHDLIVIS	DEVYEHFIYDDARHYSIAS	LDGMFERTITVNGFSKTF	AMTGW	240
Db	181	DLEEIADFVVEHDLIVIS	DEVYEHFIYDDARHYSIAS	LDGMFERTITVNGFSKTF	AMTGW	240
Qy	241	RLGFVAAPSWIIERMVKF	QMYNATCPVTFIQYAAAK	ALKDERSWKAVEEMRKEY	DRRRKL	300
Db	241	RLGFVAAPSWIIERMVKF	QMYNATCPVTFIQYAAAK	ALKDERSWKAVEEMRKEY	DRRRKL	300
Qy	301	VWKRLNEMGLPTVKPKG	AFYIFPRIRDTGLTSKKF	SELMLKEARVAVVPGSA	FGKAGEGY	360
Db	301	VWKRLNEMGLPTVKPKG	AFYIFPRIRDTGLTSKKF	SELMLKEARVAVVPGSA	FGKAGEGY	360

Qy 361 VRISYATAYEKL EAMDRM ERLK ERLV 389
| | | | | | | | | | | | | | | | | | | | | |
Db 361 VRISYATAYEKL EAMDRM ERLK ERLV 389